

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Huse, William D. Glaser, Scott M.
- (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use
- (iii) NUMBER OF SEQUENCES: 100
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell & Flores LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/016,061
 - (B) FILING DATE: 30-JAN-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/791,391
 - (B) FILING DATE: 30-JAN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-IX 2965
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..351
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg 1 10

TCC Ser	CTG Leu	AGA Arg	CTC Leu 20	TCC Ser	TGT Cys	GCA Ala	GCC Ala	TCT Ser 25	GGA Gly	TTC Phe	ACC Thr	TTC Phe	AGT Ser 30	AGC Ser	TAT Tyr	96
GAC Asp	ATG Met	TCT Ser 35	TGG Trp	GTT Val	CGC Arg	CAG Gln	GCT Ala 40	CCG Pro	GGC Gly	AAG Lys	GGT Gly	CTG Leu 45	GAG Glu	TGG Trp	GTC Val	144
GCA Ala	AAA Lys 50	GTT Val	AGT Ser	AGT Ser	GGT Gly	GGT Gly 55	GGT Gly	AGC Ser	ACC Thr	TAC Tyr	TAT Tyr 60	TTA Leu	GAC Asp	ACT Thr	GTG Val	192
CAG Gln 65	Gly	CGA Arg	TTC Phe	ACC Thr	ATC Ile 70	TCC Ser	AGA Arg	GAC Asp	AAT Asn	AGT Ser 75	AAG Lys	AAC Asn	ACC Thr	CTA Leu	TAC Tyr 80	240
CTG Leu	CAA Gln	ATG Met	AAC Asn	TCT Ser 85	CTG Leu	AGA Arg	GCC Ala	GAG Glu	GAC Asp 90	ACA Thr	GCC Ala	GTG Val	TAT Tyr	TAC Tyr 95	TGT Cys	288
GCA Ala	AGA Arg	CAT His	AAC Asn 100	TAC Tyr	GGC Gly	AGT Ser	TTT Phe	GCT Ala 105	TAC Tyr	TGG Trp	GGC Gly	CAA Gln	GGG Gly 110	ACT Thr	ACA Thr	336
	ACT Thr	_														351

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser 115

(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10:3	:								
	(i)	() () ()	A) LI 3) T C) S	ENGTI YPE : FRANI	HARAC H: 32 nucl DEDNI DGY:	21 ba leic ESS:	ase p acio botl	pair: 1	5							
	(ix)		A) NA	AME/I	KEY: ION:		321									
	(xi)) SE(QUEN	CE DI	ESCR	PTI	ON:	SEQ :	ID NO	0:3:						
GAG Glu 1	ATT Ile	GTG Val	CTA Leu	ACT Thr 5	CAG Gln	TCT Ser	CCA Pro	GCC Ala	ACC Thr 10	CTG Leu	TCT Ser	CTC Leu	AGC Ser	CCA Pro 15	GGA Gly	48
GAA Glu	AGG Arg	GCG Ala	ACT Thr 20	CTT Leu	TCC Ser	TGC Cys	CAG Gln	GCC Ala 25	AGC Ser	CAA Gln	AGT Ser	ATT Ile	AGC Ser 30	AAC Asn	CAC His	96
CTA Leu	CAC His	TGG Trp 35	TAT Tyr	CAA Gln	CAA Gln	AGG Arg	CCT Pro 40	GGT Gly	CAA Gln	GCC Ala	CCA Pro	AGG Arg 45	CTT Leu	CTC Leu	ATC Ile	144
AAG Lys	TAT Tyr 50	CGT Arg	TCC Ser	CAG Gln	TCC Ser	ATC Ile 55	TCT Ser	GGG Gly	ATC Ile	CCC Pro	GCC Ala 60	AGG Arg	TTC Phe	AGT Ser	GGC Gly	192
AGT Ser 65	GGA Gly	TCA Ser	GGG Gly	ACA Thr	GAT Asp 70	TTC Phe	ACC Thr	CTC Leu	ACT Thr	ATC Ile 75	TCC Ser	AGT Ser	CTG Leu	GAG Glu	CCT Pro 80	240
GAA Glu	GAT Asp	TTT Phe	GCA Ala	GTC Val 85	TAT Tyr	TAC Tyr	TGT Cys	CAA Gln	CAG Gln 90	AGT Ser	GGC Gly	AGC Ser	TGG Trp	CCT Pro 95	CAC His	288
					ACC Thr											321
(2)	INFO	ORMA:	rion	FOR	SEQ	ID 1	NO:4	:								
•		(i) £		LEI TYI	CHAINGTH:	: 10 amin	am:	ino a id		5						
	(:	ii) N	OLE	CULE	TYPE	: pi	rote	in								
	(2	ki) S	SEQUE	ENCE	DESC	CRIP	CION	: SEÇ	O ID	NO: 4	1 :					
Glu 1	Ile	Val	Leu	Thr 5	Gln	Ser	Pro	Ala	Thr 10	Leu	Ser	Leu	Ser	Pro 15	Gly	
Glu	Arg	Ala	Thr 20	Leu	Ser	Cys	Gln	Ala 25	Ser	Gln	Ser	Ile	Ser 30	Asn	His	
Leu	His	Trp 35	Tyr	Gln	Gln	Arg	Pro 40	Gly	Gln	Ala	Pro	Arg 45	Leu	Leu	Ile	
Lys	Tyr 50	Arg	Ser	Gln	Ser	Ile 55	Ser	Gly	Ile	Pro	Ala 60	Arg	Phe	Ser	Gly	

Ser. 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Glu	Pro 80	
Glu	Asp	Phe	Ala	Val 85	Tyr	Tyr	Cys	Gln	Gln 90	Ser	Gly	Ser	Trp	Pro 95	His	
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys		Glu ,105	Ile	Lys						
(2)	INFO	ORMA'	rion	FOR	SEQ	ID 1	10:5	:								
	(i)	() (I ()	QUENCA) LE 3) TY C) SY O) TO	ENGTI (PE : [RANI	i: 35 nuc] DEDNI	51 ba Leic ESS:	ase p acio botl	pairs 1	3							
	(ix)	(2	ATURI A) NA 3) LO	AME/I			351									
	(xi)	SEÇ	QUENC	CE DI	ESCRI	[PTIC	ON: S	SEQ :	ID NO	0:5:						
GAA Glu 1.	GTG Val	CAG Gln	CTG Leu	GTG Val 5	GAG Glu	TCT Ser	GGG Gly	GGA Gly	GGC Gly 10	TTA Leu	GTG Val	AAG Lys	CCT Pro	GGA Gly 15	AGG Arg	48
TCC Ser	CTG Leu	AGA Arg	CTC Leu 20	TCC Ser	TGT Cys	GCA Ala	GCC Ala	TCT Ser 25	GGA Gly	TTC Phe	GCT Ala	TTC Phe	AGT Ser 30	AGC Ser	TAT Tyr	96
GAC Asp	ATG Met	TCT Ser 35	TGG Trp	GTT Val	CGC Arg	CAG Gln	ATT Ile 40	CCG Pro	GAG Glu	AAG Lys	AGG Arg	CTG Leu 45	GAG Glu	TGG Trp	GTC Val	144
GCA Ala	AAA Lys 50	GTT Val	AGT Ser	AGT Ser	GGT Gly	GGT Gly 55	GGT Gly	AGC Ser	ACC Thr	TAC Tyr	TAT Tyr 60	TTA Leu	GAC Asp	ACT Thr	GTG Val	192
CAG Gln 65	GGC Gly	CGA Arg	TTC Phe	ACC Thr	ATC Ile 70	TCC Ser	AGA Arg	GAC Asp	AAT Asn	GCC Ala 75	AAG Lys	AAC Asn	ACC Thr	CTA Leu	TAC Tyr 80	240
CTG Leu	CAA Gln	ATG Met	Ser	Ser	Leu	Asn	Ser	GAG Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	288
GCA Ala	AGA Arg	CAT His	AAC Asn 100	TAC Tyr	GGC Gly	AGT Ser	TTT Phe	GCT Ala 105	TAC Tyr	TGG Trp	GGC Gly	CAA Gln	GGG Gly 110	ACT Thr	CTG Leu	336
			TCT Ser													351
(2)	INFO	ORMA'	rion	FOR	SEQ	ID 1	VO:6	:								

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 117 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Lys	Pro	Gly 15	Arg	
Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Ala	Phe	Ser 30	Ser	Tyr	
Asp	Met	Ser 35	Trp	Val	Arg	Gln	Ile 40	Pro	Glu	Lys	Arg	Leu 45	Glu	Trp	Val	
Ala	Lys 50	Val	Ser	Ser	Gly	Gly 55	Gly	Ser	Thr	Tyr	Tyr 60	Leu	Asp	Thr	Val	
Gln 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ala 75	Lys	Asn	Thr	Leu	Tyr 80	
Leu	Gln	Met	Ser	Ser 85	Leu	Asn	Ser	Glu	Asp 90	Thr	Ala	Met	Tyr	Tyr 95	Cys	
Ala	Arg	His	Asn 100	Tyr	Gly	Ser	Phe	Ala 105	Tyr	Trp	Gly	Gln	Gly 110	Thr	Leu	
Val	Thr	Val 115	Ser	Ala												
(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:7	:								
	(i)		A) LI	ENGTI	H: 32	21 ba	ase p	pairs	3							
		į	c) s:	rani	DEDNI	leic ESS: line	both									
	(ix)) FE	ATURI	S:												
					KEY:	CDS 13	321	•								
	(xi)	SEÇ	QUENC	CE DI	ESCRI	PTIC	ON: S	SEQ I	ID NO	0:7:						
GAT Asp 1	ATT Ile	GTG Val	CTA Leu	ACT Thr 5	CAG Gln	TCT Ser	CCA Pro	GCC Ala	ACC Thr 10	CTG Leu	TCT Ser	GTG Val	ACA Thr	CCA Pro 15	GGA Gly	48
GAT Asp	AGC	GTC														
-	Ser	Val	Ser 20	CTT Leu	TCC Ser	TGC Cys	CAG Gln	GCC Ala 25	AGC Ser	CAA Gln	AGT Ser	ATT Ile	AGC Ser 30	AAC Asn	CAC His	96
CTA	CAC	Val TGG Trp 35	Ser 20 TAT	Leu	Ser	Cys	Gln TCA	Ala 25 CAT	Ser GAG	Gln TCT	Ser	Ile AGG	Ser 30 CTT	Asn	His ATC	96 144
CTA Leu	CAC His	Val TGG Trp 35	Ser 20 TAT Tyr	CAA Gln CAG	CAA Gln TCC	Cys AAA Lys ATC	TCA Ser 40	Ala 25 CAT His	Ser GAG Glu ATC	Gln TCT Ser	Ser CCA Pro	AGG Arg 45	Ser 30 CTT Leu TTC	Asn CTC Leu AGT	ATC Ile	
CTA Leu AAG Lys	CAC His TAT Tyr 50	TGG Trp 35	Ser 20 TAT Tyr TCC Ser	CAA Gln CAG Gln ACA	CAA Gln TCC Ser	Cys AAA Lys ATC Ile 55	Gln TCA Ser 40 TCT Ser	Ala 25 CAT His GGG Gly	GAG Glu ATC Ile	Gln TCT Ser CCC Pro	CCA Pro TCC Ser 60	AGG Arg AGG Arg	Ser 30 CTT Leu TTC Phe	Asn CTC Leu AGT Ser	ATC Ile GGC Gly	144
CTA Leu AAG Lys AGT Ser 65	CAC His TAT Tyr 50 GGA Gly	TGG Trp 35 CGT Arg	Ser 20 TAT Tyr TCC Ser GGG Gly	CAA Gln CAG Gln ACA Thr	CAA Gln TCC Ser GAT Asp 70 TAT	AAA Lys ATC Ile 55 TTC Phe	Gln TCA Ser 40 TCT Ser GCT Ala	Ala 25 CAT His GGG Gly CTC Leu	GAG Glu ATC Ile AGT Ser	Gln TCT Ser CCC Pro ATC Ile 75 AGT	CCA Pro TCC Ser 60 AAC Asn	AGG Arg 45 AGG Arg AGT Ser	Ser 30 CTT Leu TTC Phe GTG Val	Asn CTC Leu AGT Ser GAG Glu CCT	ATC Ile GGC Gly ACT Thr 80 CAC	144

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
		•	100	_				105		

(2) INFORMATION FOR SEQ ID NO. 0	(2)	INFORMATION	FOR	SEQ	ID	NO:8:
----------------------------------	-----	-------------	-----	-----	----	-------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His 20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile 35 40 45

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 60

Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr 65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys 100 105

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGGTGCAGC TGGTGGAGTC TGGGGGAGGC GTTGTGCAGC CTGGAAGGTC CCTGAGACTC 60
TCCTGTGCAG CCTCTGGATT CACC 84

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACTTTTGCG ACCCACTCCA GACCCTTGCC CGGAGCCTGG CGAACCCAAG ACATGTCATA 60
GCTACTGAAG GTGAATCCAG AGGC 84

(2) INFORMATION FOR SEQ ID NO:11:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
TGGGTCGCAA AAGTTAGTAG TGGTGGTGGT AGCACCTACT ATTTAGACAC TGTGCAGG	GC 60
CGATTCACCA TCTCCAGAGA CAATAGT	87
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
TGCACAGTAA TACACGGCTG TGTCCTCGGC TCTCAGAGAG TTCATTTGCA GGTATAGG	GT 60
GTTCTTACTA TTGTCTCTGG A	81
(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GTGTATTACT GTGCAAGACA TAACTACGGC AGTTTTGCTT ACTGGGGCCA AGGGACTA	ACA 60
GTGACTGTTT CTAGT	75
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GAGATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGA	ACT 60
CTTTCCTGCC AGGCCAGCCA AAGTATT	87
(2) INFORMATION FOR SEQ ID NO:15:	



(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GATGAGAAGC CTTGGGGCTT GACCAGGCCT TTGTTGATAC CAGTGTAGGT GGTTGCTAAT	60
ACTTTGGCTG GC	72
(2) INFORMATION FOR SEQ ID NO:16:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
CCAAGGCTTC TCATCWASTA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT	60
GGCAGTGGAT CAGGGACAGA TTTC	84
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GCTGCCACTC TGTTGACAGW AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT	60
GAGGGTGAAA TCTGTCCCTG A	81
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG	57
(2) INFORMATION FOR SEQ ID NO:19:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GCC	CAACCAG CCATGGCCGA TATTGTGCTA ACTCAG	36
(2)	INFORMATION FOR SEQ ID NO:20:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
ACA	GTTGGTG CAGCATCAGC	20
(2)	INFORMATION FOR SEQ ID NO:21:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
ACC	CCTGTGG CAAAAGCCGA AGTGCAGCTG GTGGAG	36
(2)	INFORMATION FOR SEQ ID NO:22:	
•	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
GAT	GGGGGTG TCGTTTTGGC	20
(2)	INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
GAG	ATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGACT	60
CTT?	TCCTGCC AGGCCAGCCA AAGTATT	87
(2)	INFORMATION FOR SEQ ID NO:24:	



(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
TTAGATGAGA AGCCTTGGGG CTTGACCAGG CCTTTGTTGA TACCAGTGTA GGTGGTTGCT	60
AATACTTTGG CTGGC	75
(2) INFORMATION FOR SEQ ID NO:25:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CCAAGGCTTC TCATCTAATA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT	60
GGCAGTGGAT CAGGGACAGA TTTC	84
(2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GCTGCCACTC TGTTGACAGT AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT	60
GAGGGTGAAA TCTGTCCCTG A	81
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG	57
(2) INFORMATION FOR SEQ ID NO:28:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

	Tyr 1	Pro	ту:	r Ası	o Va:	l Pro	o Asj	р Ту	r Ala	a Ser 10	r				
(2)	INFO	RMA	rion	FOR	SEQ	ID 1	NO:2	9:							
	(i)	() (I ()	A) L1 B) T C) S	CE CI ENGTI YPE: IRANI OPOLO	H: 22 nuci DEDNI	2 bas leic ESS:	se pa acid bot	airs d							
	(xi)	SEÇ	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:29	:				
GCT	ACTG	AG (GCGA!	ATCC	AG AG	3									22
(2)	INFO	RMA	rion	FOR	SEQ	ID 1	NO:3	0:							
	(i)	(1 (1 (0	A) L1 B) T C) S	CE CI ENGTI YPE: FRANI OPOLO	H: 2: nuc. DEDNI	3 bas leic ESS:	se pa acio sino	airs d							
	(ix)	(<i>)</i> (I	3) L(AME/I OCAT: THER	ION: INFO	11. ORMA	.ī3 TION	: /n	ote=			esent an Ly	codo	n	
	(xi)	SEÇ	QUEN	CE DI	ESCR	IPTIC	ON:	SEQ :	ID NO	0:30	:				
GGG	AACGA	TA 1	NNG	ATGA	SA AC	GC .									23
(2)	INFO	RMAT	rion	FOR	SEQ	ID 1	NO:3	1:							
	(i)	(2 (E	A) L1 3) T C) S	CE CI ENGTI YPE: FRANI OPOLO	H: 32 nucl	21 ba Leic ESS:	ase p acio sino	pair	s						
	(ix)	(2		E: AME/I OCATI			321								
	(xi)	SEÇ	QUEN	CE DI	ESCR:	[PTI	ON:	SEQ :	ID NO	0:31	:				
	ATT Ile														48
	AGG Arg														96
	CAC His														144

MKK Xaa	TAT Tyr 50	CGT Arg	TCC Ser	CAG Gln	TCC Ser	ATC Ile 55	TCT Ser	GGG Gly	ATC Ile	CCC Pro	GCC Ala 60	AGG Arg	TTC Phe	AGT Ser	GGC	192
						TTC Phe										240
						TAC Tyr										288
						AAG Lys										321

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His 20 25 30

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile 35 40 45

Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGA TTC ACC TTC AGT AGC TAT GAC ATG TCT
Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

113

- (2) INFORMATION FOR SEQ ID NO:34: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGG GTC GCA AAA GTT AGT AGT GGT GGT Trp Val Ala Lys Val Ser Ser Gly Gly Gly 30

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp Val Ala Lys Val Ser Ser Gly Gly Gly

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: 30 AGC ACC TAC TAT TTA GAC ACT GTG CAG GGC Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly 1 5 (2) INFORMATION FOR SEQ ID NO:38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38: Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly (2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39: GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC 30 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr (2) INFORMATION FOR SEQ ID NO:40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(A) NAME/KEY: CDS

(ix) FEATURE:

(B) LOCATION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAG GCC AGC CAA AGT ATT AGC AAC CAC CTA CAC TGG TAT Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr

39

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr 1 5 10

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..33
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTT CTC ATC CGT TAT CGT TCC CAG TCC ATC TCT Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser 1

33

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..27 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: 27 CAA CAG AGT GGC AGC TGG CCT CAC ACG Gln Gln Ser Gly Ser Trp Pro His Thr 5 (2) INFORMATION FOR SEQ ID NO:46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: Gln Gln Ser Gly Ser Trp Pro His Thr 1 (2) INFORMATION FOR SEQ ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both
(D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: GGA ACT ACC TTC AGT AGC TAT GAC ATG TCT 30 Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48: Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser

117

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both

(D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49: 30 GGA TTC ACC TGG AGT AGC TAT GAC ATG TCT Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser (2) INFORMATION FOR SEQ ID NO:50: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50: Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser (2) INFORMATION FOR SEQ ID NO:51: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..30 . (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51: GGA TTC ACC TTC CTG AGC TAT GAC ATG TCT 30 Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser (2) INFORMATION FOR SEQ ID NO:52: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser

(2) INFORMATION FOR SEQ ID NO:53:

118 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: 30 TGG GTC GCA AAA GTT AAA AGT GGT GGT Trp Val Ala Lys Val Lys Ser Gly Gly Gly (2) INFORMATION FOR SEQ ID NO:54: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: Trp Val Ala Lys Val Lys Ser Gly Gly Gly 5 (2) INFORMATION FOR SEQ ID NO:55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55: AGC ACC TAC TAT CCT GAC ACT GTG CAG GGC Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly 30 (2) INFORMATION FOR SEQ ID NO:56: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly

- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AGC ACC TAC TAT TTA GAC ACT GTG GAG GGC Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly 30

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly 1

- (2) INFORMATION FOR SEQ ID NO:59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCA AGA CAT AAC CAT GGC AGT TTT GCT TAC Ala Arg His Asn His Gly Ser Phe Ala Tyr 5 1

- (2). INFORMATION FOR SEQ ID NO:60:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60: Ala Arg His Asn His Gly Ser Phe Ala Tyr (2) INFORMATION FOR SEQ ID NO:61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61: GCA AGA CAT AAC TAC GGC AGT TAT GCT TAC Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr 30 (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr (2) INFORMATION FOR SEQ ID NO:63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63: GCA AGA CAT AAC TAC GGC AGT TTT GAT TAC 30 Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr (2) INFORMATION FOR SEQ ID NO:64:

12

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

(A) LENGTH: 10 amino acids (B) TYPE: amino acid

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: both

 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCA AGA CAT AAC TAC GGC AGT TTT TAT TAC Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr 30

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCA AGA CAT AAC TAC GGC AGT TTT GCT TCT Ala Arg His Asn Tyr Gly Ser Phe Ala Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:68:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Arg His Asn Tyr Gly Ser Phe Ala Ser

- (2) INFORMATION FOR SEQ ID NO:69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCA AGA CAT AAC TAC GGC AGT TTT GCT ACT Ala Arg His Asn Tyr Gly Ser Phe Ala Thr 1

30

- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids

 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ala Arg His Asn Tyr Gly Ser Phe Ala Thr

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GAT Ala Arg His Asn Tyr Gly Ser Phe Ala Asp

- (2) INFORMATION FOR SEQ ID NO:72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala Arg His Asn Tyr Gly Ser Phe Ala Asp

- (2) INFORMATION FOR SEQ ID NO:73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GAG Ala Arg His Asn Tyr Gly Ser Phe Ala Glu 10 1

30

- (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Arg His Asn Tyr Gly Ser Phe Ala Glu

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCA AGA CAT AAC TAC GGC AGT TTT GCT ATG Ala Arg His Asn Tyr Gly Ser Phe Ala Met

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala Arg His Asn Tyr Gly Ser Phe Ala Met

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GGG Ala Arg His Asn Tyr Gly Ser Phe Ala Gly 1

30

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ala Arg His Asn Tyr Gly Ser Phe Ala Gly

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GCT 30 Ala Arg His Asn Tyr Gly Ser Phe Ala Ala (2) INFORMATION FOR SEQ ID NO:80: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: Ala Arg His Asn Tyr Gly Ser Phe Ala Ala (2) INFORMATION FOR SEQ ID NO:81: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81: 39 CAG GCC AGC CAA AGT ATT AGC AAC TTT CTA CAC TGG TAT Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr 1 (2) INFORMATION FOR SEQ ID NO:82: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82: Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr (2). INFORMATION FOR SEQ ID NO:83: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE:

126

(A) NAME/KEY: CDS(B) LOCATION: 1..33

33

27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83: CTT CTC ATC CGT TAT TCT TCC CAG TCC ATC TCT Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser 1 (2) INFORMATION FOR SEQ ID NO:84: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84: Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser (2) INFORMATION FOR SEQ ID NO:85: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..27 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85: CAA CAG AGT AAT AGC TGG CCT CAC ACG Gln Gln Ser Asn Ser Trp Pro His Thr (2) INFORMATION FOR SEQ ID NO:86: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86: Gln Gln Ser Asn Ser Trp Pro His Thr (2) INFORMATION FOR SEQ ID NO:87: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CAA CAG AGT ACT AGC TGG CCT CAC ACT Gln Gln Ser Thr Ser Trp Pro His Thr 5

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Gln Gln Ser Thr Ser Trp Pro His Thr 5 1

- (2) INFORMATION FOR SEQ ID NO:89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..27
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAA CAG AGT GGC AGC TGG CCT CTG ACG Gln Gln Ser Gly Ser Trp Pro Leu Thr 1

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gln Gln Ser Gly Ser Trp Pro Leu Thr

- (2) INFORMATION FOR SEQ ID NO:91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

27

(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..27 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91: CAA CAG AGT GGC AGC TGG CCT CAG ACG Gln Gln Ser Gly Ser Trp Pro Gln Thr 27 (2) INFORMATION FOR SEQ ID NO:92: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92: Gln Gln Ser Gly Ser Trp Pro Gln Thr 5 (2) INFORMATION FOR SEQ ID NO:93: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93: GCA AGA CAT AAC CAT GGC AGT TTT GCT TCT 30 Ala Arg His Asn His Gly Ser Phe Ala Ser 1 (2) INFORMATION FOR SEQ ID NO:94: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94: Ala Arg His Asn His Gly Ser Phe Ala Ser

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GCA AGA CAT AAC CAT GGC AGT TTT TAT TCT Ala Arg His Asn His Gly Ser Phe Tyr Ser 30

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ala Arg His Asn His Gly Ser Phe Tyr Ser

- (2) INFORMATION FOR SEQ ID NO:97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCA AGA CAT AAC TAC GGC AGT TTT TAT GAG Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu 30

- (2) INFORMATION FOR SEQ ID NO:98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both

 - (D) TOPOLOGY: linear
- (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCA AGA CAT AAC TAC GGC AGT TTT TAT TCT Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser

30

- (2) INFORMATION FOR SEQ ID NO:100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser 5